

SeqServer®

biology in silico

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Translation

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PF-0066-2DIVSCAH-2
gi|1363129|pir|D48909

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO: 2

Sequence 2: gi|1363129|pir|D48909

161 aa Wilkie et al. GPCR8

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 8

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:744

Alignment Score -27

CLUSTAL-Alignment file created [baa08rUyK.aln]

CLUSTAL W (1.7) multiple sequence alignment

PF-0066-2DIVSCAH-2 -----MKAVLLALLMAGLALQPGTALLCYSCKAQVSNE
gi|1363129|pir|D48909 VGVRLSLKYPALMTTERKAAAILALLWVALVSVGPLLGWKEPVPPDERF

*.:**** * : . ** :

PF-0066-2DIVSCAH-2 CLQVENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDSDQYYVGKKN-
gi|1363129|pir|D48909 CGITEEVGYAIFSSVCSFYLPMAVIVVMYCRVYVVARSTTRSLEAGIKRE

* .*: . . : .:****: : . . : . * *

PF-0066-2DIVSCAH-2 -----ITCCDLDLCNX-----SGAHALQPAAILALLPALGLL
gi|1363129|pir|D48909 PGKASEVVLRIHCRGAATSAKGNPGTQSSKGHTLRSSLSVRLKFSREKK

* * .: . * .:****: : * :

PF-0066-2DIVSCAH-2 LWGPGQL----
gi|1363129|pir|D48909 AAKTLAIVGV

. :

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PF-0066-2DIVSCAH-2
gi|478299|pir||JN0831

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO: 2

Sequence 2: gi|478299|pir||JN0831

267 aa Wray and Fisher GlnR

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 13

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:747

Alignment Score -2

CLUSTAL-Alignment file created [baa0fhJdp.aln]

CLUSTAL W (1.7) multiple sequence alignment

```
PF-0066-2DIVSCAH-2      -----MKAVLLALLMAGLALQPGTALLCYSCKAQVSNE
gi|478299|pir||JN0831    MSSLLLLTNALQPSTEVLPALGLLHNVVAPAEGLVDTGADVILVD
                          : *: * * . : * * . * : : :
```

```
PF-0066-2DIVSCAH-2      ---DCLQVENCTQLG---EQCWTARIRAVGLLTVISKGCSLNCVDDSDQ
gi|478299|pir||JN0831    GRRDLPQIRSLCQLLRSTGLSCPLVLIVTEGGLAAVTADWGIDDVLLDTA
                          * * : . . * * . * : * * : : . : : * .
```

```
PF-0066-2DIVSCAH-2      -----YYVGKKNITCCDLDLCNXSGAHALQPAAILALLPALGLL
gi|478299|pir||JN0831    GPAEVEARLRLATGRQQLGGDDSPMEIRNGDLSVDEATYSAKLKGRVLDL
                          . * : : : * : : . * : : : * : : *
```

```
PF-0066-2DIVSCAH-2      LWGPGQL-----
gi|478299|pir||JN0831    TFKEFELLKYLAQHPRGVFTRAQLLQEVWGYDYFGGTRTVDVHVRRLRAK
                          : : *
```

```
PF-0066-2DIVSCAH-2      -----
gi|478299|pir||JN0831    LGPEHESLIGTVRNVGYRFVTPEKPEKGEKSDKSEKAERA EKAERAETPG
```

PF-0066-2DIVSCAH-2

gi|478299|pir||JN0831

KAAAETNEAAGARSSKV

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 PF-0066-2DIVSCAH-2
 gi|730069|sp|Q08326|MSS4_RAT

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO:2

Sequence 2: gi|730069|sp|Q08326|MSS4_RAT

123 aa Burton et al. MSS4

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 5

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:715

Alignment Score 23

CLUSTAL-Alignment file created [baa0L2OjI.aln]

CLUSTAL W (1.7) multiple sequence alignment

PF-0066-2DIVSCAH-2
gi|730069|sp|Q08326|MSS4_RAT

MKAVLLALLMAGLALQPGTALLCYSCAQVSNECLQVENCTQLGEQCWT
MEPCELQNELVSAEGRNRKAVLCQRCGSRV-----LQPGTALFSRRQLFL
*:. * :.. : .*: * :.* ** .. .*

PF-0066-2DIVSCAH-2
gi|730069|sp|Q08326|MSS4_RAT

ARIRAVGLLTVIS--KGCSLNCVDDSDYYVGK-----KNITCC
PSMRKKPDLVDGSDPDGVLEEHVLVNDMFIENVGFTKDVGNVFLVCA
. : * . * . * * : : * : : * : . *

PF-0066-2DIVSCAH-2
gi|730069|sp|Q08326|MSS4_RAT

DTDLCNXSGAHALQAAAILALLPALGLLLWGPGQL
DCEIGP-IGWHCLDDKNSFYVALERSHE-----
* : : * * . * : : . * : .

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PF-0066-2DIVSCAH-2

gi|530797|gb|AAA20877.1|

CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO:2

Sequence 2: gi|530797|gb|AAA20877.1|

88 aa Birkeland ~~et al.~~ LysA

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 13

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:538

Alignment Score 12

CLUSTAL-Alignment file created [baa9Wed__.aln]

CLUSTAL W (1.7) multiple sequence alignment

PF-0066-2DIVSCAH-2
gi|530797|gb|AAA20877.1|

```
MKAVLLALLMAG----LALQPGTALLCYSCAQVSNECLQVENCTQLGE
MNQINWKLRLKSKAFWLALLPALFLLIQAIGASFG-----YKWNFVILNQ
*: : * : . *** * . ** : *... * . *..
```

PF-0066-2DIVSCAH-2
gi|530797|gb|AAA20877.1|

```
QCWTARIRAVGLLTVISKGCSLNCVDDSDYVVGKN-ITCCDTDLNXXS
QLAAVVNAAFALLAIV--G----VVADPTTSGLGSDRVLNKKSEENK-
* :. *...*: : * * . :*... : *.. *
```

PF-0066-2DIVSCAH-2
gi|530797|gb|AAA20877.1|

```
GAHALQPAAAILALLPALGLLLWGPGQL
-----
```

Submit sequences to:

**IncyteGenomics**

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>